

Page 1, after the title, insert the following new paragraph:

This is a continuation of application Serial No. 08/362,455, filed January 11, 1995, which is a 371 application of PCT/EP94/01323, filed April 27, 1994, the entire content of which is hereby incorporated by reference in this application.

Page 33, delete the paragraph spanning lines 28-33 and insert the following therefor:

- M44, Q70, A87, N106, K115, V137, G142, P165, I178, F251, A299, N303, Q317 which are specific for the Core/E1 region of the HCV type 45 sequence of the present invention as shown in Fig. 5;

Page 39, delete the paragraphs spanning lines 11-33 and insert the following therefor:

- a sequence having a homology of more than 80%, preferably more than 82%, most preferably more than 84% homology to any of the amino acid sequences as represented in SEQ ID NO 119, 121, and 123 119, 121, and 123 (GB358, GB549, GB809 sequences) in the region spanning positions 127 to 319 of the Core/E1 region as shown in Figure 5;

- a sequence having a homology of more than 73%, preferably more than 75%, most preferably more than 78% homology in the E1 region spanning positions 192 to 319 to any of the amino acid sequences as represented in SEQ ID NO 118, 120, and 122 119, 121, and 123 (GB358, GB549, GB809 sequences) in the region spanning positions 140 to 319 of the Core/E1 region as shown in Figure 5;

- a sequence having more than 85%, preferably more than 86%, most preferably more than 87% homology to any of the amino acid sequences as represented in SEQ ID NO ~~118, 120 or 122~~119, 121, or 123 (GB358, GB549, GB809 sequences) in the region spanning positions 192 to 319 of E1 as shown in Figure 5;
- a sequence showing more than 73%, preferably more than 74%, most preferably more than 75% homology to any of the amino acid sequences as represented in SEQ ID NO ~~106, 108, 110, 112, 114 or 116~~107, 109, 111, 113, 115 or 117 (GB48, GB116, GB215, GB358, GB549, GB809 sequences) in the region spanning positions 2645 to 2757 of the NS5B region as shown in Figure 2;
- a sequence having any of the sequences as represented in SEQ ID NO 164 or 166 (GB809 and CAM600 sequences) in the Core-E1 region as shown in Figure 5;
- a sequence having any of the sequences as represented in SEQ ID NO 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188 or 190 (CAM600, GB809, CAMG22, CAMG27, GB549, GB438, CAR4/1205, CAR4/901, GB116, GB215, GB958, GB809-4 sequences) in the Core/E1 region as shown in Figure 5;

*H3 cancel*  
Page 40, delete the paragraph spanning lines 1-3 and insert the following therefor:

*H4*

- a sequence having any of the sequences as represented in SEQ ID NO ~~192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212~~ (GB358, GB724, BE100, PC, CAM600, CAMG22, etc.) in the NS5B region or in SEQ ID NOS: 198, 200 in the NS3/4 region.

Page 40, delete the paragraph spanning lines 22-25 and insert the following  
therefor:

HS - a sequence having more than 90%, preferably more than 91%, most  
preferably more than 92% homology to any of the amino acid sequences represented in  
SEQ ID NO 56 ~~to or~~ 58 (PC sequences) in the region spanning positions 1286 to 1403 of  
the NS3 region as shown in Figure 7 or 11;

Page 51, delete the paragraphs spanning lines 27-30 and insert the following  
therefor:

Hb For the NS3/NS4 border region, the following sets of primers were selected in  
the regions of little sequence variability after aligning the sequences of HCV-1 (Choo et  
al., 1991), HCV-J (Kato et al., 1990), HC-J6 (Okamoto et al., 1991), and HC-J8  
(Okamoto et al., 1992) (smaller case lettering is used for nucleotides added for cloning  
purposes):